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Homology modeling of pyranose 2-oxidase from *Phanerochaete chrysosporium* (Article)

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Abstract

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Currently, most of the demand for energy relies on petroleum products. Nevertheless, the issues of energy security, economics and environment has led to the breakthrough of biofuel cells (BFCs) technology as one of the promising solution to the problems. However, the performance of BFCs need to be improved in order to compete with the existing technologies. One way to improve the efficiency of BFCs is to ensure that the enzyme used as the catalyst in BFCs, in this case, pyranose 2-oxidase (P2Ox) has better binding characteristic and more reactive. For this purpose, studies on three-dimensional (3-D) structure of P2Ox enzyme can offer insights on the structure-function correlations. Unfortunately, at present there is no available crystal structure of P2Ox from *Phanerochaete chrysosporium* (PcP2Ox). Thus, in this study homology modelling was used as the reliable alternative method to predict the 3-D structure of PcP2Ox enzyme and thus provide necessary information to improve the efficiency of the enzyme.

Author keywords

Homology modelling Phanerochaete chrysosporium Pyranose-2-oxidase

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